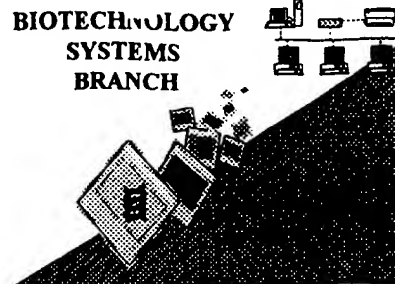


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/766,889

Source: OIPE

Date Processed by STIC: 2/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPF

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/766,889

DATE: 02/06/2001
TIME: 15:50:33

Input Set : A:\507830_1.txt

Output Set: N:\CRF3\02062001\I766889.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Luiten, Rosalie
 4 Eoon-Falleur, Thierry
 5 van der Bruggen, Pierre
 6 Strobant, Vincent
 7 Demotte, Nathalie
 8 Schultz, Erwin
 10 <120> TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
 12 <130> FILE REFERENCE: L0461/7104
 14 <140> CURRENT APPLICATION NUMBER: US/09/766,889
 14 <141> CURRENT FILING DATE: 2001-01-19
 14 <150> PRIOR APPLICATION NUMBER: US 60/177,242
 15 <150> PRIOR APPLICATION NUMBER: US 60/243,212
 16 <160> NUMBER OF SEQ ID: 59
 18 <170> SOFTWARE: FastSEQ for Windows Version 3.0

insert hard return after each response

ERRORS SEQUENCES

277 <210> SEQ ID NO: 24
 278 <211> LENGTH: 9
 279 <212> TYPE: PRT
 280 <213> ORGANISM: Homo sapiens
 282 <400> SEQUENCE: 24
 283 Val Leu Pro Asp Val Phe Ile Arg Cys
 --> 284 1

5 5
*misaligned amino acid nos. - see item 4 on Error
 summary sheet*

See following pages for more errors

<210> 53
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 53

Xaa₁ Glu Ala Asp Pro Thr Gly His Ser Tyr
 5 10

see item 10 on Ena Summary Sheet

09/9 889

3

insert a hard return after each response

<210> 55
 <211> 314
 <400> 55

<212> PRT

<213> Homo sapiens

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
 1 5 10 15
 Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
 20 25 30
 Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Thr Leu Val Glu Val
 35 40 45
 Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser
 50 55 60
 Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
 65 70 75 80
 Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Gly Pro Ser
 85 90 95
 Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
 100 105 110
 Val Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
 115 120 125
 Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
 130 135 140
 Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu
 145 150 155 160
 Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr
 165 170 175
 Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
 180 185 190
 Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile
 195 200 205
 Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
 210 215 220
 Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Leu Gly
 225 230 235 240
 Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn Tyr Leu
 245 250 255
 Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
 260 265 270
 Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His
 275 280 285
 His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu
 290 295 300
 His Glu Trp Val Leu Arg Glu Gly Glu Glu
 305 310

<210> 56
 <400> 56

<211> 9

<212> PRT

<213> Homo sapiens

Glu Val Asp Pro Ile Gly His Leu Tyr
 1 5

*These format errors appear in seqs. 55
 through 59*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/766,889

DATE: 02/06/2001

TIME: 15:50:34

Input Set : A:\507830_1.txt

Output Set: N:\CRF3\02062001\I766889.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:15 M:289 W: Numeric Identifier Missing or Out-Of-Order, <150> PRIOR APP FILING DATE
 L:16 M:283 W: Missing Blank Line separator, <160> field identifier
 L:284 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24
 L:544 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:53
 L:544 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:53
 L:544 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:53
 L:544 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:53
 L:544 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:53
 L:551 M:283 W: Missing Blank Line separator, <400> field identifier
 L:571 M:282 W: Numeric Field Identifier Missing, <212> is required.
 L:571 M:282 W: Numeric Field Identifier Missing, <213> is required.
 L:571 M:283 W: Missing Blank Line separator, <400> field identifier
 L:615 M:282 W: Numeric Field Identifier Missing, <211> is required.
 L:615 M:282 W: Numeric Field Identifier Missing, <212> is required.
 L:615 M:282 W: Numeric Field Identifier Missing, <213> is required.
 L:615 M:283 W: Missing Blank Line separator, <400> field identifier
 L:620 M:282 W: Numeric Field Identifier Missing, <211> is required.
 L:620 M:282 W: Numeric Field Identifier Missing, <212> is required.
 L:620 M:282 W: Numeric Field Identifier Missing, <213> is required.
 L:620 M:283 W: Missing Blank Line separator, <400> field identifier
 L:625 M:282 W: Numeric Field Identifier Missing, <211> is required.
 L:625 M:282 W: Numeric Field Identifier Missing, <212> is required.
 L:625 M:282 W: Numeric Field Identifier Missing, <213> is required.
 L:625 M:283 W: Missing Blank Line separator, <400> field identifier
 L:630 M:282 W: Numeric Field Identifier Missing, <211> is required.
 L:630 M:282 W: Numeric Field Identifier Missing, <212> is required.
 L:630 M:282 W: Numeric Field Identifier Missing, <213> is required.
 L:630 M:283 W: Missing Blank Line separator, <400> field identifier